

Resource Summary Report

Generated by SPARC SAWG on Aug 13, 2026

Penn State Institute of Computational and Data Sciences Roar Core Facility

RRID:SCR_026424

Type: Tool

Proper Citation

Penn State Institute of Computational and Data Sciences Roar Core Facility
(RRID:SCR_026424)

Resource Information

URL: <https://www.icds.psu.edu/roar-collab/>

Proper Citation: Penn State Institute of Computational and Data Sciences Roar Core Facility (RRID:SCR_026424)

Description: Provides advanced cyberinfrastructure resources including large scale compute and data storage. to the Penn State University research community under the operation of the Institute of Computational and Data Sciences

Synonyms: Roar Core Facility

Resource Type: service resource, computational service resource, core facility, access service resource

Keywords: High Performance Computing and Collaboration, cyberinfrastructure, data storage,

Availability: Restricted

Resource Name: Penn State Institute of Computational and Data Sciences Roar Core Facility

Resource ID: SCR_026424

Alternate URLs: <https://icds.psu.edu/>

Record Creation Time: 20250215T060332+0000

Record Last Update: 20260813T055346+0000

Ratings and Alerts

No rating or validation information has been found for Penn State Institute of Computational and Data Sciences Roar Core Facility.

No alerts have been found for Penn State Institute of Computational and Data Sciences Roar Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Anglero Mendez MF, et al. (2026) Natively entangled proteins are linked to human disease and pathogenic mutations likely due to a greater misfolding propensity. bioRxiv : the preprint server for biology.

Mao Y, et al. (2026) Global brain activity links subcortical degeneration to cortical tau progressively across Braak regions over early Alzheimer's disease stages. bioRxiv : the preprint server for biology.

Piao H, et al. (2026) BindPred: a framework for predicting protein-protein binding affinity from language model embeddings. Bioinformatics (Oxford, England), 42(6).

Yang Y, et al. (2026) Sensory encoding and memory retrieval are coordinated with propagating waves in the human brain. Nature communications, 17(1).

Tan SI, et al. (2026) High yield production of 3-hydroxypropionic acid using Issatchenkia orientalis. Nature communications.

Ryu EP, et al. (2026) Integrative host transcriptomic and mucosal microbiome profiling reveals region-specific host-microbiome associations across the human intestine. bioRxiv : the preprint server for biology.

Hallast P, et al. (2026) Population-scale Y chromosome assemblies reveal recurrent remodeling within constrained architectures. bioRxiv : the preprint server for biology.

Hartley AD, et al. (2026) MechFind: a computational framework for de novo prediction of enzyme mechanisms. Nature communications, 17(1).

Dutta S, et al. (2026) Accurate Coarse-Graining of Conjugated Organic Molecules in Melts and Thin Films Using Density-Dependent Potentials. Journal of chemical theory and computation, 22(7), 3697.

Formenti G, et al. (2026) The Vertebrate Genomes Project Phase I: A global reference genome resource. bioRxiv : the preprint server for biology.

Chen H, et al. (2026) Genome-wide rotational and translational phasing of nucleosomes with human transcription factors. *Molecular cell*, 86(14), 2722.

Hu M, et al. (2025) Parameterization of cell-free systems with time-series data using KETCHUP. *PLoS computational biology*, 21(11), e1013724.

Hartley AD, et al. (2025) MechFind: A computational framework for de novo prediction of enzyme mechanisms. *bioRxiv : the preprint server for biology*.

Amoah EI, et al. (2025) FloralArea: AI-powered algorithm for automated calculation of floral area from flower images to support plant and pollinator research. *PloS one*, 20(9), e0332165.

Willis TC, et al. (2025) Reconstruction of a resource balance analysis model of *Clostridium thermocellum* examines the metabolic cost of glycolytic and cellulosome enzymes. *Metabolic engineering*, 93, 14.